Limited influence of hospital wastewater on the microbiome and resistome of wastewater in a community sewerage system

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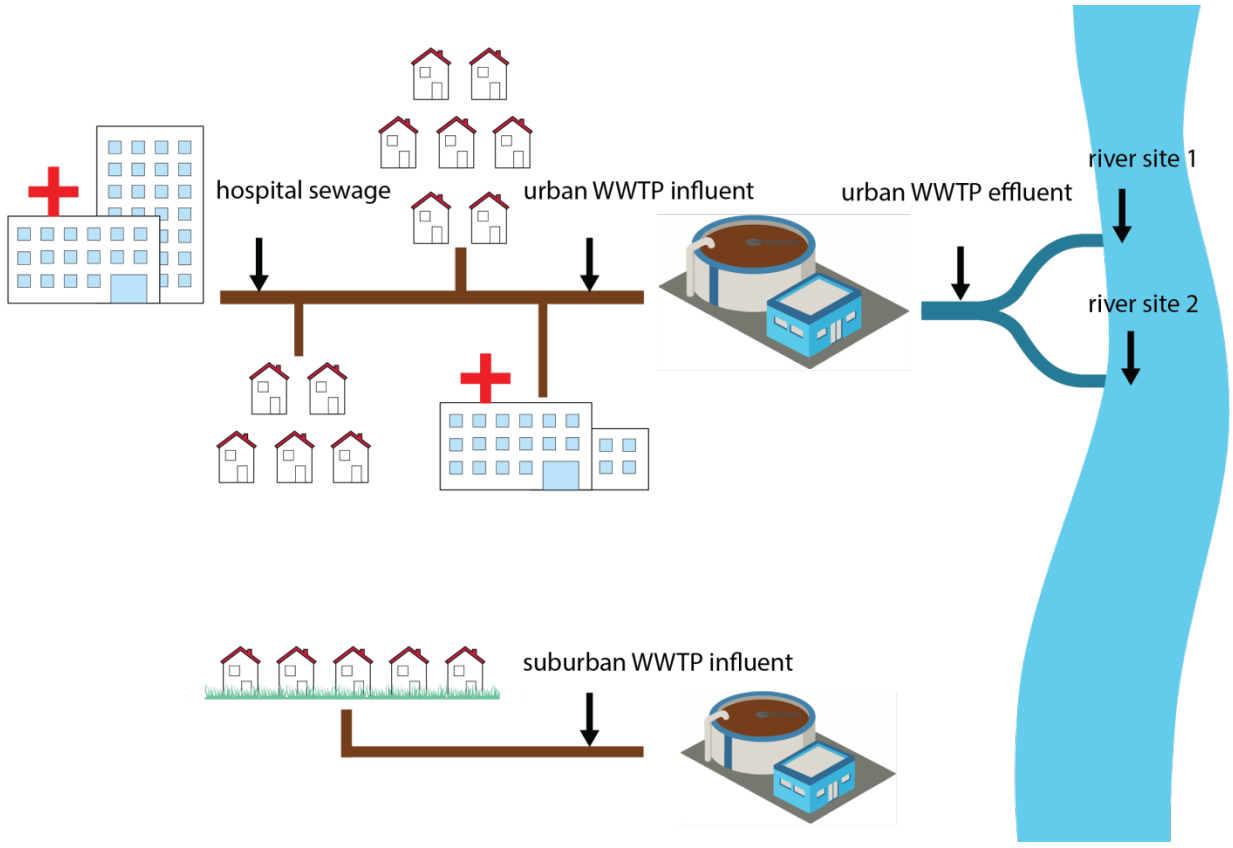
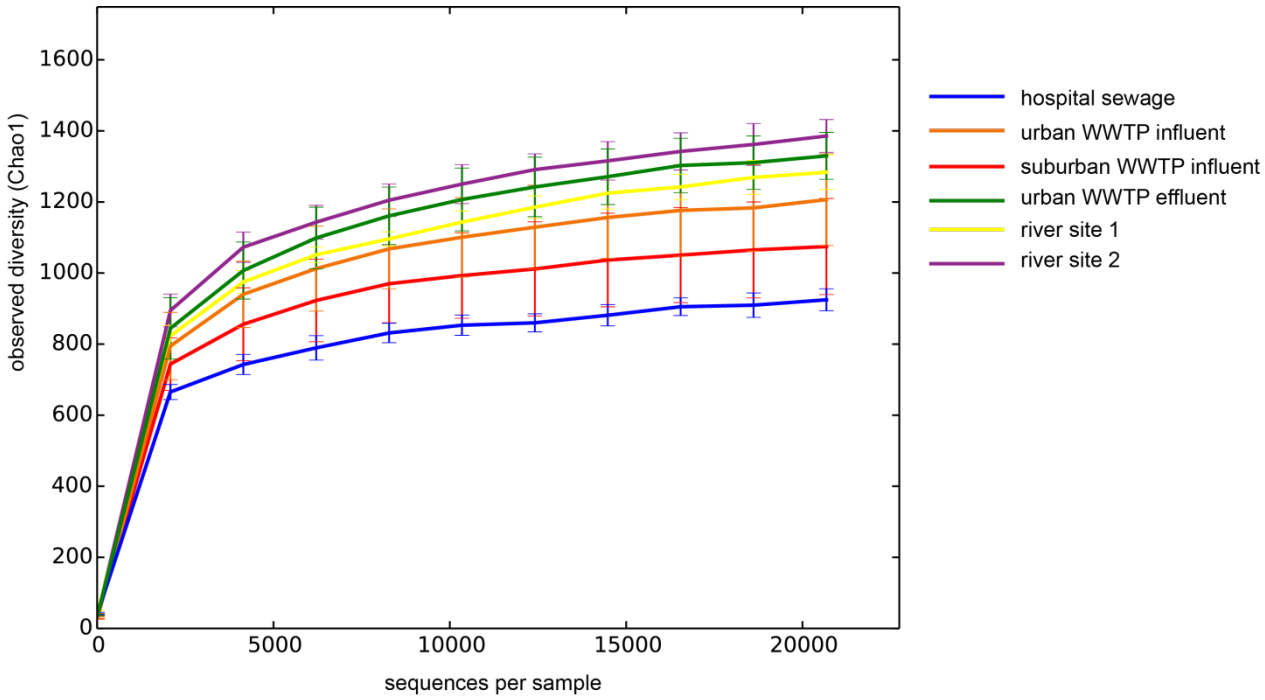
Supplementary Figures and Tables



Supplementary Figure 1: Schematic representation of sampling locations. Sampling was carried out on four different days within the course of 2.5 weeks (Monday 31 March 2014; Wednesday 2 April 2014; Monday 7 April 2014; Monday 14 April 2014). The different sampling locations are indicated by black arrows. The vector graph depicting the sewage treatment plant was provided by Tracey Saxby, Integration and Application Network, University of Maryland Center for Environmental Science.



Supplementary Figure 2: Observed diversity for the different sampling sites. Rarefaction curves depict the Chao1 index which indicates the species diversity per sampling site as a function of the sub-sampling depth with the maximum threshold of 20681 sequences per sample.

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Supplementary Table 1. Primers used in this study. Primers were developed to target the indicated ARGs. Primer sequences in bold indicate ARGs which were detected in ≥1 sample. Grey background indicates modifications to primer sequences compared to those published in Buelow *et al.*, 2017.

Antimicrobial resistance gene	Accession number	Forward primer	Reverse primer
catB3	**ABD58915.1**	**AAGGCAAGCTGCTTTCTGAG**	**TCGAATGAGTGCCCATGATA**
acrF	**CAR04877.2**	**ACTGACACCGGTTGATGTGA**	**GAGCAATAATCGAGGCGTTC**
tolC	**BAG78840.1**	**CTGAAAGAAGCCGAAAAACG**	**CGTCGGTAAGTGACCATCCT**
acrA	**ACI36997.1**	**GAAGGTAGCGACATCGAAGC**	**CTTTCGCCAGATCACCTTTC**
aph(3')-III	**ACB90577.1**	**CCGGTATAAAGGGACCACCT**	**CTTTGGAACAGGCAGCTTTC**
aph(2")-Ib	**AF207840.1**	**ATCAAATCCCTGCGGTAGTG**	**CAAGGGCATCCTTTTCCTTT**
***aadE*-like gene**	**AAW34138.1**	**GCATGATTTCCTGGCTGATT**	**CCACAATTCCTCTGGGACAT**
aac(6')-aph(2")	**ABY79711.1**	**TCCAAGAGCAATAAGGGCATA**	**TGCCCTCGTGTAATTCATGT**
aac(6')-Ii	WP_002293989.1	AGACAGCTCGGCAGAAGAAG	ACCGTATTGAGGGATTGCAC
aac(3')-Ii(acde)	**HQ246166.1**	**TGACGTATGAGATGCCGATG**	**GAGAATGCCGTTTGAATCGT**
aac(6')-Ib	**KM387722.1**	**TTGCAATGCTGAATGGAGAG**	**TGGTCTATTCCGCGTACTCC**
aadA	**ADW23165.1**	**CAGCGGAGGAATTCTTTGAC**	**GCTGCGAGTTCCATAGCTTC**
aac(6')-IIa	**ACR24243.1**	**GGAACACTACCTGCCCAGAG**	**GCGACGTACGACTGAGCATA**
aph(2")-I(de)	**AAC14693.1**	**CGGAGGTGGTTTTTACAGGA**	**TTGCTTCGGCAGATTATTGA**
aph(3')-Ia, -Ic	**CAQ58482.1**	**ATTCTCACCGGATTCAGTCG**	**GATTCCGACTCGTCCAACAT**
strB	**CAJ77026.1**	**GGCGATTATAGCCGATCAAA**	**CGCGACTGGAGAACATGATA**
bacA_2	**ABR38862.1**	**GAGGCATTGATCCTTGGTGT**	**AAACAATGCCGAACCGATAG**
bacA_1	**CAH05846.1**	**GGCTGCGTTACTGTCGTTTT**	**GGCCAATGATAAATGCATCC**
bacA	ACL18936.1	AACTTCCCGTTCTGGTGCTA	CATAACGGGGATAGCGAGAA
***bla*$_{GES}$**	**ABG47465.1**	**GACCCACACCATTGAGAGGT**	**GCGCAGGTACCAGTTTTCTC**
***bla*$_{IMP}$**	**AJ640197.1**	**GCTACCGCAGCAGAGTCTTT**	**CCCACCCGTTAACTTCTTCA**
bla$_{VIM}$	AM183120.1	TGTCCGTGATGGTGATGAGT	TTTCAATCTCCGCGAGAAGT
***bla*$_{ACC}$**	**AJ870923.1**	**TTGTTACGCTACGTGCAAGC**	**CGATTTGAAATAGCCGGTGT**
***bla*$_{DHA}$**	**AHN96243.1**	**AAAGTGCGCAAAGCCAGTAT**	**AAGATTCCGCATCAAGCTGT**
bla$_{IMI}$	U50278.1	AGTCGATCCCAGCAGCTTTA	CCAAGAAACTGTGCATTCCA
bla$_{CMY-1/MOX}$	AF357598.1	GATCTGCTGCGTTTTGTGAA	CTACCGAGTAATGCCCTTGG
***bla*$_{AMPC}$**	**ABF06289.1**	**ACCGCTAAACAGTGGAATGG**	**GCAAGTCGCTTGAGGATTTC**
cepA	**CR626927.1**	**ATGTCCTGCCCTGGTAGTTG**	**CTTGCCCGTCGATAATGACT**
cepA_2	AE016945.1	TGCACCAAGACGAAAGTCTG	ACAGTGCTTCTTTGCGGAAT
bla$_{BIC-1}$	GQ260093.1	CCATCAGCGCACAACATAGT	CCAGAACGTTTTCCAGAAGC
cblA	**AAA66962.1**	**TGCCTGCGACATCTTGATAG**	**CCGTCTTCTGTTTCCGAGAG**
cfxA	**AY769933.1**	**GCGCAAATCCTCCTTTAACA**	**ACAATAACCGCCACACCAAT**
***bla*$_{CMY-2}$**	**AAZ99133.1**	**CGATCCGGTCACGAAATACT**	**CCTGCCGTATAGGTGGCTAA**
***bla*$_{CTX-M}$**	**ABG46354.1**	**ACTATGGCACCACCAACGAT**	**GGTTGAGGCTGGGTGAAGTA**
***bla*$_{TEM}$**	**NP_775035.1**	**AAGCCATACCAAACGACGAG**	**TTGCCGGGAAGCTAGAGTAA**
***bla*$_{SHV}$**	**AAV83796.1**	**CTTTCCCATGATGAGCACCT**	**CAGATCCTGCTGGCGATAGT**
***bla*$_{NDM}$**	**CAZ39946.1**	**TGGATCAAGCAGGAGATCAA**	**ATTGGCATAAGTCGCAATCC**
***bla*$_{OXA}$**	**AAP70012.1**	**GTGGCATCGATTATCGGAAT**	**AGAGCACAACTACGCCCTGT**
bla$_{KPC}$	AEL12451.1	TGGCTAAAGGGAAACACGAC	TAGTCATTTGCCGTGCCATA
cat	**ABO92401.1**	**CAATCCTCAATCGACACGAA**	**GATTGTGTAGCAAGGCAGCA**
mdtL	**CAR15381.2**	**CGGACAAACCACGAGAAAAT**	**GAAGGTGAGGATCACCGAAA**
mdtF	**KEL93478.1**	**GGACCCGCAAAAACTCAATA**	**AGTTGACCACCGGAAATCTG**

Antimicrobial resistance gene	Accession number	Forward primer	Reverse primer
ermF	BAD66041.1	AGCACCCGCTTTTTCCTTAT	GATCAAGAGGGGCTTTAGGG
ermB	**BAH18720.1**	**GGTTGCTCTTGCACACTCAA**	**CTGTGGTATGGCGGGTAAGT**
ermG	122586.NMB0066	TGCTGTCTTTTACAGGCCACT	GCATATGTTCCAGTCCCTTCA
ermC	**BAE05991.1**	**TGAAATCGGCTCAGGAAAAG**	**GGTCTATTTCAATGGCAGTTACG**
mefA_10	**583346.CKR_2320**	**CCTGCAAATGGCGATTATTT**	**CCAAAGACCGCATAGGGTAA**
mefA_3	**286636.M6_SPY1166**	**TTACCCTATGCGGTCTTTGG**	**GAACCAGCTGCTGCGATAAT**
macB	**ACR63203.1**	**GGCTGGAAGACCGTACAGAG**	**GTTGGTTCATCGGCAAGAAT**
fosB	NP_372857.1	AGCTTGCAGGCCTATGGAT	TGCCAATATTTAAATTCGCTGTC
cfr	YP_003896025.1	CAAACGAAGGGCAGGTAGAA	GACCACAAGCAGCGTCAATA
mfsA	**WP_002584949.1**	**AATATGCTCTCCGGGCTTTT**	**TTTGCACACCGTAAAATGGA**
ermA	AB047088.2	GAGGGGTTTACCGCTTCTTT	ATCGGATCAGGAAAAGGACA
mecA	YP_184944.1	TCCAGGAATGCAGAAAGACC	GGCCAATTCCACATTGTTTC
arnA	**CAR03684.2**	**GAAATTCACCGTCTGGTCGT**	**GTGGTGCAACAGAAATCACG**
mdtO	**ASB78387.1**	**TTGTTGGCCTCTATCCAACC**	**TTAAGCGCTTGATGCATTTG**
qacA	**YP_536864**	**GACCCTTCTGGTACCCAACA**	**TCCCCATTTATCAGCAAAGG**
qacC	**CAA86016.1**	**TGGGCGGGACTAGGTTTAG**	**ACGAAACTACGCCGACTATGA**
cm1A1	**ABI50481.1**	**AATGGGATGCCTGATAGCTG**	**ACCCACTAGCCACATTGGAG**
qacE	**NC_001735.4**	**TCGGTGTTGCTTATGCAGTC**	**ATCAAGCTTTTGCCCATGAA**
qnrA	**ACA43024.1**	**ATTTCTCACGCCAGGATTTG**	**ACTGCAATCCTCGAAACTGG**
qnrB	**AFD54601.1**	**CGATCTGACCAATTCGGAGT**	**ACGATGCCTGGTAGTTGTCC**
qnrC	ACK75961.1	GCAGAATTCAGGGGTGTGAT	AACTGCTCCAAAAGCTGCTC
qnrS	**AEG74318.1**	**TGGAAACCTACCGTCACACA**	**AATCGCATCGGATAAAGGTG**
spc	**AAL05549.1**	**TGACGAACGCAATGTGATTT**	**TCAGCTGCCAGATCTTTTGA**
vatA	AAF24087.1	AACAGCTTCTGCAGCAATGA	CCTTGAAAGGGGACATTGAA
vatB	**AAA86871.1**	**TGGGAAAAAGCAACTCCATC**	**TTCTGACCAATCCACACATCA**
aadE	**CAZ55809.1**	**TGTGCCGCAAAGAGATACTG**	**AACCTTCCACGACATCATCC**
sul1	**ADB23338.1**	**AGGCTGGTGGTTATGCACTC**	**AAGAACCGCACAATCTCGTC**
tetQ	**Y08615.1**	**GCAAAGGAAGGCATACAAGC**	**AAACGCTCCAAATTCACACC**
tetX	ABQ05845.1	CGGTACGCTGGATTTACACA	CATCGGAATTGCCTTTTTGT
tetW	**ACD97480.1**	**GGTGCAGTTGGAGGTTGTTT**	**AAATGACGGAGGGTTCCTTT**
tetM	**ACO22036.1**	**TTGATGCGGGAAAAACTACC**	**TACCTCTGTCCACGCTTCCT**
tetO	**EAQ71799.1**	**GCGTCAAAGGGGAATCACTA**	**CGGTATACTTCCGCCAAAAA**
tetB	**AAL09908.1**	**CAAAACTTGCCCCTAACCAA**	**GCTTTCAGGGATCACAGGAG**
dfrA27	**ACD45689.1**	**TTGTTGTTTCTGGTGGTGGA**	**TTCCGGAAAGAAAACATTGC**
dfrF	**AEBU01000146.1**	**GATTGTTGCGAGGTCAAAGAA**	**CGCCCCATAATAACCACATT**
vanUG	ACR77286.1	ATTTGCGAAACTCGGAAAAA	ACACCTCATTTTCGGGTACG
vanR	CAJ68489.1	TGAAGCTGTATGGGGAGAAAA	TTTCGGGTTTTTAGAAGGTTCA
vanA	**ACP19236.1**	**GTGCGGTATTGGGAAACAGT**	**TGCGTTTTCAGAGCCTTTTT**
vanB	**WP_032489746.1**	**CCTGCCTGGTTTTACATCGT**	**GCTGTCAATCAGTGCAGGAA**
vanX	**NP_878017.1**	**CCGGTTGACGGTTATGAAGT**	**CAGCCAGTTCTTTTGCCTTC**
cfr_2	AJ249217.1	GCCGGAGCTTTTCCTCTACT	GGTGCCGAAAGTCAAAACAT
sulA	**AAB03082.1**	**GATATTCGCGGTTTTCCAGAACC**	**GTCTTGCACCGAATGCATAAC**
16S rRNA	a	**CAACGCGARGAACCTTACC**	**ACAACACGAGCTGACGAC**

a The primers for the 16S rRNA gene were previously described by Gloor *et al*. (2010), PLoS ONE 5(10): e15406. doi:10.1371/journal.pone.0015406

Supplementary Table 2. Results 16S rRNA gene profiling (aggregated to order level). Numbers represent the abundance, as percentage of the total microbiome, of each indicated taxa.

	hospital sewage t1	hospital sewage t2	hospital sewage t3	hospital sewage t4	urban WWTP influent t1	urban WWTP influent t2	urban WWTP influent t3	urban WWTP influent t4	suburban WWTP influent t1	suburban WWTP influent t2	suburban WWTP influent t3	suburban WWTP influent t4
Clostridiales	29.50	27.42	27.41	30.42	26.94	13.34	17.65	14.53	18.40	21.10	19.63	16.84
Lactobacillales	15.18	18.49	16.99	9.31	15.23	20.57	8.61	7.43	10.85	9.42	8.69	14.43
Pseudomonadales	8.03	7.01	4.99	7.95	9.21	3.92	5.25	2.05	4.58	4.55	3.82	3.39
Bacteroidales	6.88	7.57	4.35	5.92	4.33	5.78	4.19	2.24	5.36	5.19	7.34	3.65
Burkholderiales	6.87	5.32	9.08	7.47	5.59	3.26	5.35	6.16	4.73	4.94	5.10	4.38
Aeromonadales	4.96	6.70	3.78	4.15	2.16	19.29	11.11	9.91	13.06	7.54	11.43	17.26
Actinomycetales	3.86	2.29	4.04	5.14	5.02	3.42	3.59	3.35	4.12	3.03	3.97	4.67
Campylobacterales	3.77	6.08	5.63	6.61	4.31	10.06	17.55	29.03	16.95	15.13	18.24	12.36
Bifidobacteriales	3.71	4.36	4.21	4.82	5.34	2.05	3.77	2.57	2.68	2.30	3.06	2.46
Coriobacteriales	2.67	2.50	2.81	2.89	2.85	1.43	2.41	2.15	1.72	1.77	1.98	2.00
Flavobacteriales	1.43	0.90	1.76	1.64	0.76	0.33	0.79	0.46	0.39	0.93	0.37	0.28
Rhodocyclales	1.31	0.89	1.57	1.42	1.36	2.49	2.57	3.54	3.48	3.05	3.91	3.21
Enterobacteriales	1.11	1.24	1.58	1.27	1.41	1.94	2.00	1.45	1.46	1.60	1.56	1.95
Rhodobacterales	0.83	0.37	1.04	0.78	1.04	0.21	0.66	0.66	0.34	0.72	0.28	0.37
Neisseriales	0.73	0.64	0.99	0.72	0.65	0.33	0.70	0.89	0.41	0.64	0.64	0.42
Rhizobiales	0.52	0.39	0.70	0.60	0.64	0.17	0.47	0.54	0.23	0.59	0.20	0.24
Xanthomonadales	0.50	0.22	0.60	0.50	0.33	0.09	0.26	0.37	0.12	0.30	0.13	0.12
Fusobacteriales	0.48	0.14	0.12	0.31	1.07	1.99	1.79	0.52	1.82	2.49	1.08	2.08
Erysipelotrichales	0.47	0.49	0.89	0.61	0.59	0.12	0.21	0.30	0.38	0.23	0.21	0.21
Desulfovibrionales	0.32	0.28	0.38	0.37	0.29	0.59	0.39	0.24	0.61	0.36	0.81	0.67
ASSO-13-(Rhodocyclales)	0.32	0.26	0.49	0.22	0.29	0.07	0.30	0.48	0.15	0.29	0.13	0.12
Synergistales	0.27	0.09	0.05	0.16	0.98	0.79	0.98	0.98	0.92	2.15	1.24	1.25
Unassigned	3.77	4.85	3.95	4.27	4.03	5.56	4.42	4.77	4.91	4.29	3.82	5.14
others	2.48	1.48	2.58	2.45	5.55	2.20	4.96	5.36	2.31	7.39	2.37	2.48

	urban effluent t1	urban effluent t2	urban effluent t3	urban effluent t4	river water site 1 t1	river water site 1 t2	river water site 1 t3	river water site 1 t4	river water site 2 t1	river water site 2 t2	river water site 2 t3	river water site 2 t4
Clostridiales	9.83	10.70	7.24	11.31	6.28	3.75	6.13	5.94	6.65	8.45	7.78	9.21
Lactobacillales	1.42	2.85	1.06	2.09	1.10	0.97	1.04	1.22	1.32	0.94	1.58	1.55
Pseudomonadales	0.89	2.72	0.60	0.79	0.37	0.57	0.32	0.46	0.66	0.90	0.83	1.04
Bacteroidales	1.95	1.73	1.12	2.11	0.66	0.83	1.11	1.40	1.25	1.25	1.67	2.35
Burkholderiales	12.56	13.08	10.98	8.45	14.40	11.96	8.17	8.32	9.41	12.89	11.97	7.66
Aeromonadales	1.17	1.98	0.65	1.23	0.43	0.28	0.58	1.07	0.77	0.67	1.48	1.69
Actinomycetales	12.08	23.05	18.25	19.38	13.50	11.93	17.20	17.91	17.09	16.85	14.27	17.41
Campylobacterales	2.71	2.63	1.28	3.46	1.63	0.97	0.93	1.41	0.92	1.91	3.15	3.27
Bifidobacteriales	0.61	0.47	0.46	0.83	0.58	0.37	0.43	0.58	0.55	0.48	0.54	0.77
Coriobacteriales	0.67	1.00	0.53	0.93	0.41	0.30	0.47	0.43	0.54	0.53	0.84	0.84
Flavobacteriales	0.44	10.96	0.46	0.40	0.38	0.56	0.53	0.58	0.42	0.41	0.50	0.49
Rhodocyclales	7.46	4.69	9.52	8.69	13.89	16.47	12.32	13.90	9.49	7.81	9.79	8.48
Enterobacteriales	0.46	0.59	0.30	0.89	0.18	0.13	0.18	0.29	0.38	0.31	0.40	0.68
Rhodobacterales	0.56	0.32	0.96	0.80	0.87	1.56	1.48	1.60	1.42	0.79	0.96	0.95
Neisseriales	1.97	0.18	1.32	0.78	1.04	0.82	0.49	0.41	0.75	1.89	1.33	0.55
Rhizobiales	1.05	0.44	1.40	1.28	1.31	2.04	1.96	2.26	1.76	1.14	1.39	1.47
Xanthomonadales	0.30	0.28	0.56	0.39	0.72	0.86	0.71	0.82	0.47	1.37	0.54	0.50
Fusobacteriales	0.22	0.16	0.12	0.06	0.02	0.05	0.13	0.07	0.08	0.11	0.13	0.08
Erysipelotrichales	0.08	0.08	0.03	0.11	0.03	0.04	0.05	0.05	0.06	0.05	0.10	0.12
Desulfovibrionales	0.10	0.20	0.11	0.18	0.06	0.03	0.06	0.08	0.09	0.09	0.15	0.13
ASSO-13 (Rhodocyclales)	0.02	0.01	0.01	0.03	0.05	0.04	0.03	0.06	0.03	0.03	0.04	0.07
Synergistales	0.22	0.22	0.34	0.36	0.15	0.05	0.33	0.18	0.22	0.20	0.10	0.32
Unassigned	3.97	3.59	3.59	3.65	1.88	3.32	3.03	2.94	3.68	3.72	3.51	2.90
others	39.26	18.05	39.10	31.80	40.05	42.08	42.30	38.01	41.99	37.20	36.93	37.46

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Supplementary Table 3: Aggregated cumulative abundance of ARG classes relative to the 16S rRNA gene.

	aminoglycosides	bacitracin	β-lactams	chloramphenicols	efflux	macrolides	polymyxins
hospital sewage t1	1429.19	11.30	513.11	20.76	47.37	361.11	2.11
hospital sewage t2	1423.39	12.57	568.49	20.60	47.32	375.27	2.15
hospital sewage t3	1660.78	12.89	605.79	16.78	51.58	403.89	2.15
hospital sewage t4	1633.67	12.06	590.51	20.00	46.05	358.19	1.75
urban WWTP influent t1	87.02	5.83	38.72	9.31	27.77	163.60	0.92
urban WWTP influent t2	247.49	4.23	27.49	14.39	15.23	235.73	0.86
urban WWTP influent t3	106.03	3.46	41.34	15.22	21.21	107.09	0.92
urban WWTP influent t4	159.04	4.49	45.60	20.35	25.42	134.69	0.96
suburban WWTP influent t1	124.07	3.30	30.57	10.86	18.79	64.30	0.70
suburban WWTP influent t2	119.86	7.26	43.60	13.32	23.07	135.36	0.86
suburban WWTP influent t3	118.46	5.28	37.64	9.23	18.83	164.84	0.77
suburban WWTP influent t4	193.30	3.02	32.04	15.53	21.74	232.83	1.07
urban WWTP effluent t1	34.35	2.74	14.75	1.95	4.60	20.79	0.24
urban WWTP effluent t2	36.57	1.48	10.30	1.88	3.72	24.04	0.27
urban WWTP effluent t3	25.47	1.63	10.03	1.48	2.69	11.21	ND
urban WWTP effluent t4	43.17	5.00	23.40	3.43	7.61	27.53	0.40
river water site 1 t1	29.28	2.37	10.27	1.47	3.90	22.08	0.23
river water site 1 t2	25.94	0.97	4.82	0.38	1.64	15.71	ND
river water site 1 t3	26.28	1.39	7.29	0.98	2.48	14.97	ND
river water site 1 t4	30.90	1.84	10.63	1.74	3.47	19.36	ND
river water site 2 t1	18.36	2.30	9.70	1.37	3.39	13.78	ND
river water site 2 t2	39.02	2.35	10.50	1.41	3.23	19.80	0.20
river water site 2 t3	39.99	2.57	14.78	2.04	4.62	19.37	ND
river water site 2 t4	58.06	4.57	26.27	4.12	7.35	31.70	0.42

	QAC resistance genes	quinolones	streptogramins	sulphonamides	tetracyclines	trimethoprim	vancomycin
hospital sewage t1	344.47	9.17	ND	216.50	384.68	12.17	386.38
hospital sewage t2	337.67	6.91	0.07	214.56	387.78	14.31	302.88
hospital sewage t3	388.42	7.15	ND	234.68	402.38	11.04	377.20
hospital sewage t4	371.23	6.61	ND	243.17	390.20	15.34	457.12
urban WWTP influent t1	45.50	5.58	1.38	29.45	238.76	10.80	2.03
urban WWTP influent t2	93.93	6.87	0.90	59.21	197.41	2.41	ND
urban WWTP influent t3	82.65	4.96	1.34	54.48	186.89	5.54	1.81
urban WWTP influent t4	88.49	7.14	1.43	59.19	180.66	6.47	3.63
suburban WWTP influent t1	10.83	7.56	1.11	8.26	86.37	4.59	0.00
suburban WWTP influent t2	68.33	6.05	1.62	45.47	215.08	4.66	3.30
suburban WWTP influent t3	77.72	4.90	1.10	47.07	209.39	3.82	0.29
suburban WWTP influent t4	93.17	5.59	1.30	58.94	189.38	3.93	0.18
urban WWTP effluent t1	60.35	0.91	0.00	38.49	45.90	1.43	0.00
urban WWTP effluent t2	25.52	0.81	0.00	17.44	47.16	0.77	1.31
urban WWTP effluent t3	70.48	0.45	0.00	43.60	30.13	0.79	0.00
urban WWTP effluent t4	76.09	2.39	0.00	54.03	70.46	1.79	0.00
river water site 1 t1	53.19	0.80	ND	35.46	39.29	1.17	ND
river water site 1 t2	61.59	0.32	ND	43.29	23.08	0.68	0.25
river water site 1 t3	60.13	0.33	ND	49.54	30.12	0.92	ND
river water site 1 t4	67.05	0.81	ND	49.71	35.37	0.96	ND
river water site 2 t1	56.33	0.57	ND	42.26	33.41	0.79	ND
river water site 2 t2	71.04	0.76	ND	45.97	42.81	0.87	0.76
river water site 2 t3	68.26	0.74	ND	52.54	45.71	1.25	ND
river water site 2 t4	90.82	1.82	ND	59.42	63.83	2.15	1.49

Abundance for each individual ARG was calculated relative to the CT-value of 16S rRNA in each sample, as described in the Materials and Methods. Abundances of each ARG detected per ARG class were then aggregated to determine the relative abundance of ARG classes. ND: not detectable.

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